



SEQUENCE LISTING

<110> Martelange, Valerie
De Smet, Charles
Boon-Falleur, Thierry

<120> TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR

<130> L0461.70047US00

<150> US 09/183,789

<151> 1998-10-30

<150> US 09/060,706

<151> 1998-04-15

<160> 47

<170> PatentIn version 3.2

<210> 1

<211> 204

<212> DNA

<213> Homo sapiens

<400> 1

gatcggttgta cctcttcaag caaaatgaaa attctttcat aattttgccc aaaccttcga 60

acttctttca ttaattgata ttttatatca tcattaattt tctttgccat ggcaggagat 120

atttggtgtg tatttggcac agtttcaccg aagacattac tgtaactggt gggtcacgtg 180

cagagacact gtagtttttg gtgc 204

<210> 2

<211> 20

<212> DNA

<213> Homo sapiens

<400> 2

tgtacctctt caagcaaat 20

<210> 3

<211> 20

<212> DNA

<213> Homo sapiens

<400> 3

gtgaccacc agttacagta 20

<210> 4

<211> 9

<212> PRT

<213> Homo sapiens

<400> 4

Glu Ala Asp Pro Thr Gly His Ser Tyr
1 5

<210> 5

<211> 9

<212> PRT

<213> Homo sapiens

<400> 5

Ser Ala Tyr Gly Glu Pro Arg Lys Leu
1 5

<210> 6

<211> 9

<212> PRT

<213> Homo sapiens

<400> 6

Glu Val Asp Pro Ile Gly His Leu Tyr
1 5

<210> 7

<211> 9

<212> PRT

<213> Homo sapiens

<400> 7

Phe Leu Trp Gly Pro Arg Ala Leu Val
1 5

<210> 8

<211> 10

<212> PRT

<213> Homo sapiens

<400> 8

Met Glu Val Asp Pro Ile Gly His Leu Tyr
1 5 10

<210> 9

<211> 9

<212> PRT

<213> Homo sapiens

<400> 9

Ala Ala Arg Ala Val Phe Leu Ala Leu
1 5

<210> 10
<211> 8
<212> PRT
<213> Homo sapiens

<400> 10

Tyr Arg Pro Arg Pro Arg Arg Tyr
1 5

<210> 11
<211> 10
<212> PRT
<213> Homo sapiens

<400> 11

Ser Pro Ser Ser Asn Arg Ile Arg Asn Thr
1 5 10

<210> 12
<211> 9
<212> PRT
<213> Homo sapiens

<400> 12

Val Leu Pro Asp Val Phe Ile Arg Cys
1 5

<210> 13
<211> 10
<212> PRT
<213> Homo sapiens

<400> 13

Val Leu Pro Asp Val Phe Ile Arg Cys Val
1 5 10

<210> 14
<211> 9
<212> PRT
<213> Homo sapiens

<400> 14

Glu Glu Lys Leu Ile Val Val Leu Phe

1 5

<210> 15
<211> 9
<212> PRT
<213> Homo sapiens

<400> 15

Glu Glu Lys Leu Ser Val Val Leu Phe
1 5

<210> 16
<211> 10
<212> PRT
<213> Homo sapiens

<400> 16

Ala Cys Asp Pro His Ser Gly His Phe Val
1 5 10

<210> 17
<211> 10
<212> PRT
<213> Homo sapiens

<400> 17

Ala Arg Asp Pro His Ser Gly His Phe Val
1 5 10

<210> 18
<211> 9
<212> PRT
<213> Homo sapiens

<400> 18

Ser Tyr Leu Asp Ser Gly Ile His Phe
1 5

<210> 19
<211> 9
<212> PRT
<213> Homo sapiens

<400> 19

Ser Tyr Leu Asp Ser Gly Ile His Ser
1 5

<210> 20
<211> 9
<212> PRT
<213> Homo sapiens

<400> 20

Met Leu Leu Ala Val Leu Tyr Cys Leu
1 5

<210> 21
<211> 9
<212> PRT
<213> Homo sapiens

<400> 21

Tyr Met Asn Gly Thr Met Ser Gln Val
1 5

<210> 22
<211> 9
<212> PRT
<213> Homo sapiens

<400> 22

Ala Phe Leu Pro Trp His Arg Leu Phe
1 5

<210> 23
<211> 9
<212> PRT
<213> Homo sapiens

<400> 23

Ser Glu Ile Trp Arg Asp Ile Asp Phe
1 5

<210> 24
<211> 9
<212> PRT
<213> Homo sapiens

<400> 24

Tyr Glu Ile Trp Arg Asp Ile Asp Phe
1 5

<210> 25

<211> 15
<212> PRT
<213> Homo sapiens

<400> 25

Gln Asn Ile Leu Leu Ser Asn Ala Pro Leu Gly Pro Gln Phe Pro
1 5 10 15

<210> 26
<211> 15
<212> PRT
<213> Homo sapiens

<400> 26

Asp Tyr Ser Tyr Leu Gln Asp Ser Asp Pro Asp Ser Phe Gln Asp
1 5 10 15

<210> 27
<211> 10
<212> PRT
<213> Homo sapiens

<400> 27

Glu Ala Ala Gly Ile Gly Ile Leu Thr Val
1 5 10

<210> 28
<211> 9
<212> PRT
<213> Homo sapiens

<400> 28

Ala Ala Gly Ile Gly Ile Leu Thr Val
1 5

<210> 29
<211> 9
<212> PRT
<213> Homo sapiens

<400> 29

Ile Leu Thr Val Ile Leu Gly Val Leu
1 5

<210> 30
<211> 9
<212> PRT

<213> Homo sapiens

<400> 30

Lys Thr Trp Gly Gln Tyr Trp Gln Val
1 5

<210> 31

<211> 9

<212> PRT

<213> Homo sapiens

<400> 31

Ile Thr Asp Gln Val Pro Phe Ser Val
1 5

<210> 32

<211> 9

<212> PRT

<213> Homo sapiens

<400> 32

Tyr Leu Glu Pro Gly Pro Val Thr Ala
1 5

<210> 33

<211> 10

<212> PRT

<213> Homo sapiens

<400> 33

Leu Leu Asp Gly Thr Ala Thr Leu Arg Leu
1 5 10

<210> 34

<211> 10

<212> PRT

<213> Homo sapiens

<400> 34

Val Leu Tyr Arg Tyr Gly Ser Phe Ser Val
1 5 10

<210> 35

<211> 9

<212> PRT

<213> Homo sapiens

<400> 35

Leu Tyr Val Asp Ser Leu Phe Phe Leu
1 5

<210> 36

<211> 12

<212> PRT

<213> Homo sapiens

<400> 36

Lys Ile Ser Gly Gly Pro Arg Ile Ser Tyr Pro Leu
1 5 10

<210> 37

<211> 9

<212> PRT

<213> Homo sapiens

<400> 37

Tyr Met Asp Gly Thr Met Ser Gln Val
1 5

<210> 38

<211> 2021

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (119)..(1831)

<400> 38

ctcactatag ggagaccac gcttggtacc gagctcgat ccactagtaa cggccgccag 60

tgtgctggaa agtgttcaac cagtgattat ttatttgaca gcaactggta ttccgggc 118

atg aat acc agg gat cag tat gct acc atc act cac aat gtc tgt gaa 166

Met Asn Thr Arg Asp Gln Tyr Ala Thr Ile Thr His Asn Val Cys Glu
1 5 10 15

gag aga gtg gta aat aac caa cca cta cct agt aac gcc ttg tca act 214

Glu Arg Val Val Asn Asn Gln Pro Leu Pro Ser Asn Ala Leu Ser Thr
20 25 30

gtt cta cca ggg ctt gct tat ttg gca aca gct gat atg cca gcc atg 262

Val Leu Pro Gly Leu Ala Tyr Leu Ala Thr Ala Asp Met Pro Ala Met
35 40 45

agt acc agg gat cag cat gct acc atc att cac aat ctg cgt gaa gag 310

Ser Thr Arg Asp Gln His Ala Thr Ile Ile His Asn Leu Arg Glu Glu

50	55	60	
aag aaa gat aac agc caa cca acc cct gat aac gtc ttg tca gct gtt Lys Lys Asp Asn Ser Gln Pro Thr Pro Asp Asn Val Leu Ser Ala Val 65 70 75 80			358
aca cca gag ctt att aac ttg gca gga gct ggt att cca ccc atg agt Thr Pro Glu Leu Ile Asn Leu Ala Gly Ala Gly Ile Pro Pro Met Ser 85 90 95			406
acc agg gat cag tat gct acc gtc aat cac cat gtc cat gaa gca agg Thr Arg Asp Gln Tyr Ala Thr Val Asn His His Val His Glu Ala Arg 100 105 110			454
atg gaa aat ggc caa cga aaa cag gat aac gtc ttg tca aat gtt cta Met Glu Asn Gly Gln Arg Lys Gln Asp Asn Val Leu Ser Asn Val Leu 115 120 125			502
tcc ggg ctt att aat atg gca gga gct agt att cca gca atg agt tcc Ser Gly Leu Ile Asn Met Ala Gly Ala Ser Ile Pro Ala Met Ser Ser 130 135 140			550
agg gat ctg tat gct acc att act cac agt gtt cgt gaa gag aag atg Arg Asp Leu Tyr Ala Thr Ile Thr His Ser Val Arg Glu Glu Lys Met 145 150 155 160			598
gaa agt ggc aaa ccc cag act gat aag gtc ata tca aat gat gca cca Glu Ser Gly Lys Pro Gln Thr Asp Lys Val Ile Ser Asn Asp Ala Pro 165 170 175			646
cag ctt ggt cat atg gct gca ggt ggt att cca tcc atg agt acc aag Gln Leu Gly His Met Ala Ala Gly Gly Ile Pro Ser Met Ser Thr Lys 180 185 190			694
gat ctg tat gct acc gtc act caa aat gtc cat gaa gag agg atg gaa Asp Leu Tyr Ala Thr Val Thr Gln Asn Val His Glu Glu Arg Met Glu 195 200 205			742
aat aac caa cca caa cct agt tat gac ttg tca act gtt cta cca gga Asn Asn Gln Pro Gln Pro Ser Tyr Asp Leu Ser Thr Val Leu Pro Gly 210 215 220			790
ctt act tat ttg aca gta gct ggt att ccg gcc atg agt acc agg gat Leu Thr Tyr Leu Thr Val Ala Gly Ile Pro Ala Met Ser Thr Arg Asp 225 230 235 240			838
cag tat gct acc gtc act cac aat gtc cat gaa gag aag att aaa aat Gln Tyr Ala Thr Val Thr His Asn Val His Glu Glu Lys Ile Lys Asn 245 250 255			886
ggc caa gca gca tcc gat aat gtc ttc tcg act gtt cca cca gca ttt Gly Gln Ala Ala Ser Asp Asn Val Phe Ser Thr Val Pro Pro Ala Phe 260 265 270			934
att aat atg gca gca act ggt gtt tca tcc atg agt acc agg gat cag Ile Asn Met Ala Ala Thr Gly Val Ser Ser Met Ser Thr Arg Asp Gln 275 280 285			982

tat gct gca gtc act cac aac atc cgt gaa gag aag ata aat aac agc Tyr Ala Ala Val Thr His Asn Ile Arg Glu Glu Lys Ile Asn Asn Ser 290 295 300	1030
caa cca gca cct ggt aac atc ttg tca act gct cct cca tgg ctt cgt Gln Pro Ala Pro Gly Asn Ile Leu Ser Thr Ala Pro Pro Trp Leu Arg 305 310 315 320	1078
cat atg gca gca gct gga att tca tcc acg att acc agg gat ctg tat His Met Ala Ala Gly Ile Ser Ser Thr Ile Thr Arg Asp Leu Tyr 325 330 335	1126
gtc acc gcc act cac agt gtc cat gag gag aag atg aca aat ggc caa Val Thr Ala Thr His Ser Val His Glu Glu Lys Met Thr Asn Gly Gln 340 345 350	1174
cag gca cct gat aac tcc ttg tca acg gtt cca cct ggt tgt att aat Gln Ala Pro Asp Asn Ser Leu Ser Thr Val Pro Pro Gly Cys Ile Asn 355 360 365	1222
ctg tca gga gct ggt att tca tgc aga agt acc agg gat ctg tat gct Leu Ser Gly Ala Gly Ile Ser Cys Arg Ser Thr Arg Asp Leu Tyr Ala 370 375 380	1270
act gtc att cac gat atc cag gag gag gag atg gaa aat gat caa acc Thr Val Ile His Asp Ile Gln Glu Glu Glu Met Glu Asn Asp Gln Thr 385 390 395 400	1318
cct cct gat ggc ttc ctg tca aat tct gat tca cca gag ctg ata aat Pro Pro Asp Gly Phe Leu Ser Asn Ser Asp Ser Pro Glu Leu Ile Asn 405 410 415	1366
atg aca gga cat tgt atg cca ccc aat gca ttg gat tct ttc tct cac Met Thr Gly His Cys Met Pro Pro Asn Ala Leu Asp Ser Phe Ser His 420 425 430	1414
gac ttc aca agt ctc agc aaa gat gag ctg ctt tac aaa cct gat agt Asp Phe Thr Ser Leu Ser Lys Asp Glu Leu Leu Tyr Lys Pro Asp Ser 435 440 445	1462
aat gaa ttt gcg gta ggc acc aaa aac tac agt gtc tct gca ggt gac Asn Glu Phe Ala Val Gly Thr Lys Asn Tyr Ser Val Ser Ala Gly Asp 450 455 460	1510
cca cca gtt aca gta atg tct tcg gtg gaa act gtg cca aat aca cca Pro Pro Val Thr Val Met Ser Ser Val Glu Thr Val Pro Asn Thr Pro 465 470 475 480	1558
caa ata tct cct gcc atg gca aaa aaa att aat gat gat ata aaa tat Gln Ile Ser Pro Ala Met Ala Lys Lys Ile Asn Asp Asp Ile Lys Tyr 485 490 495	1606
caa tta atg aaa gaa gtt cga agg ttt ggg caa aat tat gaa aga att Gln Leu Met Lys Glu Val Arg Arg Phe Gly Gln Asn Tyr Glu Arg Ile 500 505 510	1654

ttc att ttg ctt gaa gag gta caa gga tct atg aaa gtc aag aga caa	1702
Phe Ile Leu Leu Glu Glu Val Gln Gly Ser Met Lys Val Lys Arg Gln	
515 520 525	
ttt gtt gaa ttt acc atc aag gaa gca gca agg ttt aaa aaa gtt gtc	1750
Phe Val Glu Phe Thr Ile Lys Glu Ala Ala Arg Phe Lys Lys Val Val	
530 535 540	
tta att cag caa ctc gag aag gcg ctt aaa gaa ata gat tcc cac tgc	1798
Leu Ile Gln Gln Leu Glu Lys Ala Leu Lys Glu Ile Asp Ser His Cys	
545 550 555 560	
cat ctc aga aaa gtt aag cac atg aga aaa aga taattgtggt agtgcaaaga	1851
His Leu Arg Lys Val Lys His Met Arg Lys Arg	
565 570	
ccaaggagaa acaaggacat atgctgtagg atggaacagg ttattgctga agctccctat	1911
aatcctgaaa tgaagagaat tcccttccag aagctacgaa aaagggagct gtttaaattt	1971
aataaatctc tgtagtaaa agctgcaaaa aaaaaaaaaa aaaaaaaaaa	2021

<210> 39
 <211> 571
 <212> PRT
 <213> Homo sapiens

<400> 39

Met Asn Thr Arg Asp Gln Tyr Ala Thr Ile Thr His Asn Val Cys Glu	
1 5 10 15	
Glu Arg Val Val Asn Asn Gln Pro Leu Pro Ser Asn Ala Leu Ser Thr	
20 25 30	
Val Leu Pro Gly Leu Ala Tyr Leu Ala Thr Ala Asp Met Pro Ala Met	
35 40 45	
Ser Thr Arg Asp Gln His Ala Thr Ile Ile His Asn Leu Arg Glu Glu	
50 55 60	
Lys Lys Asp Asn Ser Gln Pro Thr Pro Asp Asn Val Leu Ser Ala Val	
65 70 75 80	
Thr Pro Glu Leu Ile Asn Leu Ala Gly Ala Gly Ile Pro Pro Met Ser	
85 90 95	
Thr Arg Asp Gln Tyr Ala Thr Val Asn His His Val His Glu Ala Arg	
100 105 110	

Met Glu Asn Gly Gln Arg Lys Gln Asp Asn Val Leu Ser Asn Val Leu
115 120 125

Ser Gly Leu Ile Asn Met Ala Gly Ala Ser Ile Pro Ala Met Ser Ser
130 135 140

Arg Asp Leu Tyr Ala Thr Ile Thr His Ser Val Arg Glu Glu Lys Met
145 150 155 160

Glu Ser Gly Lys Pro Gln Thr Asp Lys Val Ile Ser Asn Asp Ala Pro
165 170 175

Gln Leu Gly His Met Ala Ala Gly Gly Ile Pro Ser Met Ser Thr Lys
180 185 190

Asp Leu Tyr Ala Thr Val Thr Gln Asn Val His Glu Glu Arg Met Glu
195 200 205

Asn Asn Gln Pro Gln Pro Ser Tyr Asp Leu Ser Thr Val Leu Pro Gly
210 215 220

Leu Thr Tyr Leu Thr Val Ala Gly Ile Pro Ala Met Ser Thr Arg Asp
225 230 235 240

Gln Tyr Ala Thr Val Thr His Asn Val His Glu Glu Lys Ile Lys Asn
245 250 255

Gly Gln Ala Ala Ser Asp Asn Val Phe Ser Thr Val Pro Pro Ala Phe
260 265 270

Ile Asn Met Ala Ala Thr Gly Val Ser Ser Met Ser Thr Arg Asp Gln
275 280 285

Tyr Ala Ala Val Thr His Asn Ile Arg Glu Glu Lys Ile Asn Asn Ser
290 295 300

Gln Pro Ala Pro Gly Asn Ile Leu Ser Thr Ala Pro Pro Trp Leu Arg
305 310 315 320

His Met Ala Ala Ala Gly Ile Ser Ser Thr Ile Thr Arg Asp Leu Tyr
325 330 335

Val Thr Ala Thr His Ser Val His Glu Glu Lys Met Thr Asn Gly Gln
 340 345 350

Gln Ala Pro Asp Asn Ser Leu Ser Thr Val Pro Pro Gly Cys Ile Asn
 355 360 365

Leu Ser Gly Ala Gly Ile Ser Cys Arg Ser Thr Arg Asp Leu Tyr Ala
 370 375 380

Thr Val Ile His Asp Ile Gln Glu Glu Glu Met Glu Asn Asp Gln Thr
 385 390 395 400

Pro Pro Asp Gly Phe Leu Ser Asn Ser Asp Ser Pro Glu Leu Ile Asn
 405 410 415

Met Thr Gly His Cys Met Pro Pro Asn Ala Leu Asp Ser Phe Ser His
 420 425 430

Asp Phe Thr Ser Leu Ser Lys Asp Glu Leu Leu Tyr Lys Pro Asp Ser
 435 440 445

Asn Glu Phe Ala Val Gly Thr Lys Asn Tyr Ser Val Ser Ala Gly Asp
 450 455 460

Pro Pro Val Thr Val Met Ser Ser Val Glu Thr Val Pro Asn Thr Pro
 465 470 475 480

Gln Ile Ser Pro Ala Met Ala Lys Lys Ile Asn Asp Asp Ile Lys Tyr
 485 490 495

Gln Leu Met Lys Glu Val Arg Arg Phe Gly Gln Asn Tyr Glu Arg Ile
 500 505 510

Phe Ile Leu Leu Glu Glu Val Gln Gly Ser Met Lys Val Lys Arg Gln
 515 520 525

Phe Val Glu Phe Thr Ile Lys Glu Ala Ala Arg Phe Lys Lys Val Val
 530 535 540

Leu Ile Gln Gln Leu Glu Lys Ala Leu Lys Glu Ile Asp Ser His Cys
 545 550 555 560

His Leu Arg Lys Val Lys His Met Arg Lys Arg

<210> 40
 <211> 201
 <212> DNA
 <213> Homo sapiens

<400> 40
 gatctccctg aacctctact tacttttgaa tattacgaat tatttgtaaa cattttgggc 60
 ttgctgcaac ctcatctaga gagggttgcc atcgatgctc tacagttatg ttgtttgtta 120
 cttccccac caaatcgtag aaagcttcaa cttttaatgc gtatgatttc ccgaatgagt 180
 caaaatgttg atatgcccaa a 201

<210> 41
 <211> 20
 <212> DNA
 <213> Homo sapiens

<400> 41
 tctccctgaa cctctactta 20

<210> 42
 <211> 20
 <212> DNA
 <213> Homo sapiens

<400> 42
 atatcaacat ttgactcat 20

<210> 43
 <211> 2463
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (79)..(1659)

<400> 43
 gcttggtacc gagctcggat ccactagtaa cggccgccag tgtgctggaa agggacgcca 60
 ccgggcgctg acagacct atg gag agt cag ggt gtg cct ccc ggg cct tat 111
 Met Glu Ser Gln Gly Val Pro Pro Gly Pro Tyr
 1 5 10
 cgg gcc acc aag ctg tgg aat gaa gtt acc aca tct ttt cga gca gga 159
 Arg Ala Thr Lys Leu Trp Asn Glu Val Thr Thr Ser Phe Arg Ala Gly
 15 20 25

atg cct cta aga aaa cac aga caa cac ttt aaa aaa tat ggc aat tgt	207
Met Pro Leu Arg Lys His Arg Gln His Phe Lys Lys Tyr Gly Asn Cys	
30 35 40	
ttc aca gca gga gaa gca gtg gat tgg ctt tat gac cta tta aga aat	255
Phe Thr Ala Gly Glu Ala Val Asp Trp Leu Tyr Asp Leu Leu Arg Asn	
45 50 55	
aat agc aat ttt ggt cct gaa gtt aca agg caa cag act atc caa ctg	303
Asn Ser Asn Phe Gly Pro Glu Val Thr Arg Gln Gln Thr Ile Gln Leu	
60 65 70 75	
ttg agg aaa ttt ctt aag aat cat gta att gaa gat atc aaa ggg agg	351
Leu Arg Lys Phe Leu Lys Asn His Val Ile Glu Asp Ile Lys Gly Arg	
80 85 90	
tgg gga tca gaa aat gtt gat gat aac aac cag ctc ttc aga ttt cct	399
Trp Gly Ser Glu Asn Val Asp Asp Asn Asn Gln Leu Phe Arg Phe Pro	
95 100 105	
gca act tcg cca ctt aaa act cta cca cga agg tat cca gaa ttg aga	447
Ala Thr Ser Pro Leu Lys Thr Leu Pro Arg Arg Tyr Pro Glu Leu Arg	
110 115 120	
aaa aac aac ata gag aac ttt tcc aaa gat aaa gat agc att ttt aaa	495
Lys Asn Asn Ile Glu Asn Phe Ser Lys Asp Lys Asp Ser Ile Phe Lys	
125 130 135	
tta cga aac tta tct cgt aga act cct aaa agg cat gga tta cat tta	543
Leu Arg Asn Leu Ser Arg Arg Thr Pro Lys Arg His Gly Leu His Leu	
140 145 150 155	
tct cag gaa aat ggc gag aaa ata aag cat gaa ata atc aat gaa gat	591
Ser Gln Glu Asn Gly Glu Lys Ile Lys His Glu Ile Ile Asn Glu Asp	
160 165 170	
caa gaa aat gca att gat aat aga gaa cta agc cag gaa gat gtt gaa	639
Gln Glu Asn Ala Ile Asp Asn Arg Glu Leu Ser Gln Glu Asp Val Glu	
175 180 185	
gaa gtt tgg aga tat gtt att ctg atc tac ctg caa acc att tta ggt	687
Glu Val Trp Arg Tyr Val Ile Leu Ile Tyr Leu Gln Thr Ile Leu Gly	
190 195 200	
gtg cca tcc cta gaa gaa gtc ata aat cca aaa caa gta att ccc caa	735
Val Pro Ser Leu Glu Glu Val Ile Asn Pro Lys Gln Val Ile Pro Gln	
205 210 215	
tat ata atg tac aac atg gcc aat aca agt aaa cgt gga gta gtt ata	783
Tyr Ile Met Tyr Asn Met Ala Asn Thr Ser Lys Arg Gly Val Val Ile	
220 225 230 235	
cta caa aac aaa tca gat gac ctc cct cac tgg gta tta tct gcc atg	831
Leu Gln Asn Lys Ser Asp Asp Leu Pro His Trp Val Leu Ser Ala Met	
240 245 250	
aag tgc cta gca aat tgg cca aga agc aat gat atg aat aat cca act	879

Lys	Cys	Leu	Ala	Asn	Trp	Pro	Arg	Ser	Asn	Asp	Met	Asn	Asn	Pro	Thr	
			255					260					265			
tat	gtt	gga	ttt	gaa	cga	gat	gta	ttc	aga	aca	atc	gca	gat	tat	ttt	927
Tyr	Val	Gly	Phe	Glu	Arg	Asp	Val	Phe	Arg	Thr	Ile	Ala	Asp	Tyr	Phe	
		270					275					280				
cta	gat	ctc	cct	gaa	cct	cta	ctt	act	ttt	gaa	tat	tac	gaa	tta	ttt	975
Leu	Asp	Leu	Pro	Glu	Pro	Leu	Leu	Thr	Phe	Glu	Tyr	Tyr	Glu	Leu	Phe	
	285					290					295					
gta	aac	att	ttg	ggc	ttg	ctg	caa	cct	cat	tta	gag	agg	gtt	gcc	atc	1023
Val	Asn	Ile	Leu	Gly	Leu	Leu	Gln	Pro	His	Leu	Glu	Arg	Val	Ala	Ile	
300					305					310					315	
gat	gct	cta	cag	tta	tgt	tgt	ttg	tta	ctt	ccc	cca	cca	aat	cgt	aga	1071
Asp	Ala	Leu	Gln	Leu	Cys	Cys	Leu	Leu	Leu	Pro	Pro	Pro	Asn	Arg	Arg	
			320						325					330		
aag	ctt	caa	ctt	tta	atg	cgt	atg	att	tcc	cga	atg	agt	caa	aat	gtt	1119
Lys	Leu	Gln	Leu	Leu	Met	Arg	Met	Ile	Ser	Arg	Met	Ser	Gln	Asn	Val	
		335						340					345			
gat	atg	ccc	aaa	ctt	cat	gat	gca	atg	ggc	acg	agg	tca	ctg	atg	ata	1167
Asp	Met	Pro	Lys	Leu	His	Asp	Ala	Met	Gly	Thr	Arg	Ser	Leu	Met	Ile	
		350					355					360				
cat	acc	ttt	tot	cga	tgt	gtg	tta	tgc	tgt	gct	gaa	gaa	gtg	gat	ctt	1215
His	Thr	Phe	Ser	Arg	Cys	Val	Leu	Cys	Cys	Ala	Glu	Glu	Val	Asp	Leu	
	365					370					375					
gat	gag	ctt	ctt	gct	gga	aga	tta	gtt	tct	ttc	tta	atg	gat	cat	cat	1263
Asp	Glu	Leu	Leu	Ala	Gly	Arg	Leu	Val	Ser	Phe	Leu	Met	Asp	His	His	
380					385					390					395	
cag	gaa	att	ctt	caa	gta	ccc	tct	tac	tta	cag	act	gca	gtg	gaa	aaa	1311
Gln	Glu	Ile	Leu	Gln	Val	Pro	Ser	Tyr	Leu	Gln	Thr	Ala	Val	Glu	Lys	
			400						405					410		
cat	ctt	gac	tac	tta	aaa	aag	gga	cat	att	gaa	aat	cct	gga	gat	gga	1359
His	Leu	Asp	Tyr	Leu	Lys	Lys	Gly	His	Ile	Glu	Asn	Pro	Gly	Asp	Gly	
		415					420						425			
cta	ttt	gct	cct	ttg	cca	act	tac	tca	tac	tgt	aag	cag	att	agt	gct	1407
Leu	Phe	Ala	Pro	Leu	Pro	Thr	Tyr	Ser	Tyr	Cys	Lys	Gln	Ile	Ser	Ala	
		430					435					440				
cag	gag	ttt	gat	gag	caa	aaa	gtt	tct	acc	tct	caa	gct	gca	att	gca	1455
Gln	Glu	Phe	Asp	Glu	Gln	Lys	Val	Ser	Thr	Ser	Gln	Ala	Ala	Ile	Ala	
	445					450					455					
gaa	ctt	tta	gaa	aat	att	att	aaa	aac	agg	agt	tta	cct	cta	aag	gag	1503
Glu	Leu	Leu	Glu	Asn	Ile	Ile	Lys	Asn	Arg	Ser	Leu	Pro	Leu	Lys	Glu	
460					465				470						475	
aaa	aga	aaa	aaa	cta	aaa	cag	ttt	cag	aag	gaa	tat	cct	ttg	ata	tat	1551
Lys	Arg	Lys	Lys	Leu	Lys	Gln	Phe	Gln	Lys	Glu	Tyr	Pro	Leu	Ile	Tyr	

480	485	490	
cag aaa aga ttt cca acc acg gag agt gaa gca gca ctt ttt ggt gac			1599
Gln Lys Arg Phe Pro Thr Thr Glu Ser Glu Ala Ala Leu Phe Gly Asp			
495	500	505	
aaa cct aca atc aag caa cca atg ctg att tta aga aaa cca aag ttc			1647
Lys Pro Thr Ile Lys Gln Pro Met Leu Ile Leu Arg Lys Pro Lys Phe			
510	515	520	
cgt agt cta aga taactaactg aattaaaaat tatgtaatac ttgtggaact			1699
Arg Ser Leu Arg			
525			
ttgataaatg aagccatatac tgagaatgta gctactcaaa aggaagtctg tcattaataa			1759
ggatatttcta aataaacaca ttatgtaagg aagtgccaaa atagttatca atgtgagact			1819
cttaggaaac taactagatac tcaattgaga gcacataaca atagatgata ccaaatactt			1879
tttgttttta acacagctat ccagtaaggc tatcatgatg tgtgctaaaa ttttatttac			1939
ttgaattttg aaaactgagc tgtgttaggg attaaactat aattctgttc ttaaaagaaa			1999
atztatctgc aaatgtgcaa gttctgagat attagctaata gaattagttg tttgggggta			2059
cttctttggt tctaagtata agaatgtgaa gaatatttga aaactcaatg aaataattct			2119
cagctgccaa atgttgcaact cttttatata ttctttttcc acttttgatc tatttatata			2179
tatgtatgtg tttttaaaat atgtgtatat tttatcagat ttggttttgc cttaaattt			2239
atcccccaatt gcttcagtc ttcatttgtt cagtatatat attttgaatt ctagttttca			2299
taatctatta gaagatgggg atataaaaga agtataaggc aatcatatat tcattcaaaa			2359
gatatttatt tagcaactgc tatgtgcctt tcgttggttc agatatgcag agacaatgat			2419
aaataaaaca tataatctct tccaaaaaaa aaaaaaaaaa aaaa			2463

<210> 44
 <211> 527
 <212> PRT
 <213> Homo sapiens

<400> 44

Met	Glu	Ser	Gln	Gly	Val	Pro	Pro	Gly	Pro	Tyr	Arg	Ala	Thr	Lys	Leu
1				5					10					15	

Trp	Asn	Glu	Val	Thr	Thr	Ser	Phe	Arg	Ala	Gly	Met	Pro	Leu	Arg	Lys
			20					25					30		

His Arg Gln His Phe Lys Lys Tyr Gly Asn Cys Phe Thr Ala Gly Glu

35

40

45

Ala Val Asp Trp Leu Tyr Asp Leu Leu Arg Asn Asn Ser Asn Phe Gly
50 55 60

Pro Glu Val Thr Arg Gln Gln Thr Ile Gln Leu Leu Arg Lys Phe Leu
65 70 75 80

Lys Asn His Val Ile Glu Asp Ile Lys Gly Arg Trp Gly Ser Glu Asn
85 90 95

Val Asp Asp Asn Asn Gln Leu Phe Arg Phe Pro Ala Thr Ser Pro Leu
100 105 110

Lys Thr Leu Pro Arg Arg Tyr Pro Glu Leu Arg Lys Asn Asn Ile Glu
115 120 125

Asn Phe Ser Lys Asp Lys Asp Ser Ile Phe Lys Leu Arg Asn Leu Ser
130 135 140

Arg Arg Thr Pro Lys Arg His Gly Leu His Leu Ser Gln Glu Asn Gly
145 150 155 160

Glu Lys Ile Lys His Glu Ile Ile Asn Glu Asp Gln Glu Asn Ala Ile
165 170 175

Asp Asn Arg Glu Leu Ser Gln Glu Asp Val Glu Glu Val Trp Arg Tyr
180 185 190

Val Ile Leu Ile Tyr Leu Gln Thr Ile Leu Gly Val Pro Ser Leu Glu
195 200 205

Glu Val Ile Asn Pro Lys Gln Val Ile Pro Gln Tyr Ile Met Tyr Asn
210 215 220

Met Ala Asn Thr Ser Lys Arg Gly Val Val Ile Leu Gln Asn Lys Ser
225 230 235 240

Asp Asp Leu Pro His Trp Val Leu Ser Ala Met Lys Cys Leu Ala Asn
245 250 255

Trp Pro Arg Ser Asn Asp Met Asn Asn Pro Thr Tyr Val Gly Phe Glu
260 265 270

Arg Asp Val Phe Arg Thr Ile Ala Asp Tyr Phe Leu Asp Leu Pro Glu
275 280 285

Pro Leu Leu Thr Phe Glu Tyr Tyr Glu Leu Phe Val Asn Ile Leu Gly
290 295 300

Leu Leu Gln Pro His Leu Glu Arg Val Ala Ile Asp Ala Leu Gln Leu
305 310 315 320

Cys Cys Leu Leu Leu Pro Pro Pro Asn Arg Arg Lys Leu Gln Leu Leu
325 330 335

Met Arg Met Ile Ser Arg Met Ser Gln Asn Val Asp Met Pro Lys Leu
340 345 350

His Asp Ala Met Gly Thr Arg Ser Leu Met Ile His Thr Phe Ser Arg
355 360 365

Cys Val Leu Cys Cys Ala Glu Glu Val Asp Leu Asp Glu Leu Leu Ala
370 375 380

Gly Arg Leu Val Ser Phe Leu Met Asp His His Gln Glu Ile Leu Gln
385 390 395 400

Val Pro Ser Tyr Leu Gln Thr Ala Val Glu Lys His Leu Asp Tyr Leu
405 410 415

Lys Lys Gly His Ile Glu Asn Pro Gly Asp Gly Leu Phe Ala Pro Leu
420 425 430

Pro Thr Tyr Ser Tyr Cys Lys Gln Ile Ser Ala Gln Glu Phe Asp Glu
435 440 445

Gln Lys Val Ser Thr Ser Gln Ala Ala Ile Ala Glu Leu Leu Glu Asn
450 455 460

Ile Ile Lys Asn Arg Ser Leu Pro Leu Lys Glu Lys Arg Lys Lys Leu
465 470 475 480

Lys Gln Phe Gln Lys Glu Tyr Pro Leu Ile Tyr Gln Lys Arg Phe Pro
485 490 495

Thr Thr Glu Ser Glu Ala Ala Leu Phe Gly Asp Lys Pro Thr Ile Lys
500 505 510

Gln Pro Met Leu Ile Leu Arg Lys Pro Lys Phe Arg Ser Leu Arg
515 520 525

<210> 45
<211> 5726
<212> DNA
<213> Artificial

<220>
<223> unidentified cloning vector

<400> 45
gacggatcgg gagatctccc gatccccctat ggtcgactct cagtacaatc tgctctgatg 60
ccgcatagtt aagccagtat ctgctccctg cttgtgtggt ggaggtcgct gagtagtgcg 120
cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc 180
ttagggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt 240
gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata 300
tgaggttccg cgttacataa cttacggtaa atggcccggc tggctgaccg cccaacgacc 360
cccgccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 420
attgacgtca atgggtggac tatttacggg aaactgccca cttggcagta catcaagtgt 480
atcatatgcc aagtacgcc cctattgacg tcaatgacgg taaatggccc gcctggcatt 540
atgccagta catgacctta tgggactttc ctacttgga gtacatctac gtattagtca 600
tcgctattac catgggtgat cggttttgga agtacatcaa tgggcgtgga tagcggtttg 660
actcacgggg atttccaagt ctccaccca ttgacgtcaa tgggagtttg ttttggcacc 720
aaaatcaacg ggactttcca aaatgtcgta acaactccgc ccattgacg caaatgggcg 780
gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaacca 840
ctgcttactg gcttatcgaa attaatacga ctactatag ggagaccaa gcttggtacc 900
gagctcgat ccactagtaa cggccgccag tgtgctggaa ttaattcgct gtctgcgagg 960
gccagctgtt ggggtgagta ctccctctca aaagcgggca tgacttctgc gctaagattg 1020
tcagtttcca aaaacgagga ggatttgata ttcacctggc ccgcggtgat gcctttgagg 1080
gtggccgct ccatctggtc agaaaagaca atctttttgt tgtcaagctt gaggtgtggc 1140
aggcttgaga tctggccata cacttgagtg acaatgacat ccactttgcc tttctctcca 1200

caggtgtcca	ctcccaggtc	caactgcagg	tcgatcgagc	atgcatctag	ggcggccgca	1260
ctagaggaat	tcgccccctct	ccctccccc	cccctaacgt	tactggccga	agccgcttgg	1320
aataaggccg	gtgtgtgttt	gtctatatgt	gattttccac	catattgccg	tcttttggca	1380
atgtgagggc	ccggaacct	ggccctgtct	tcttgacgag	cattcctagg	ggctcttccc	1440
ctctcgccaa	aggaatgcaa	ggtctgttga	atgtcgtgaa	ggaagcagtt	cctctggaag	1500
cttcttgaag	acaaacaacg	tctgtagcga	ccctttgcag	gcagcggaac	ccccacctg	1560
gcgacaggtg	cctctgcggc	caaaagccac	gtgtataaga	tacacctgca	aaggcggcac	1620
aaccccgagt	ccacgttgtg	agttggatag	ttgtggaaag	agtcaaattg	ctctcctcaa	1680
gcgtagtcaa	caaggggctg	aaggatgcc	agaagggtacc	ccattgtatg	ggaatctgat	1740
ctggggcctc	ggtgcacatg	ctttacatgt	gtttagtcga	ggttaaaaaa	gctctaggcc	1800
ccccgaacca	cggggacgtg	gttttccttt	gaaaaacacg	atgataagct	tgccacaacc	1860
ccgtaccaaa	gatggataga	tccggaaagc	ctgaactcac	cgcgacgtct	gtcgagaagt	1920
ttctgatcga	aaagtctgac	agcgtctccg	acctgatgca	gctctcggag	ggcgaagaat	1980
ctcgtgcttt	cagcttcgat	gtaggagggc	gtggatatgt	cctgcgggta	aatagctgcg	2040
ccgatggttt	ctacaaagat	cgttatgttt	atcggcactt	tgcatcggcc	gcgctcccga	2100
ttccggaagt	gcttgacatt	ggggaattca	gcgagagcct	gacctattgc	atctcccgcc	2160
gtgcacaggg	tgtcacgttg	caagacctgc	ctgaaaccga	actgcccgct	gttctgcagc	2220
cggtcgcgga	ggccatggat	gcgatcgctg	cggccgatct	tagccagacg	agcgggttcg	2280
gccattcgg	accgcaagga	atcgggtcaat	acactacatg	gcgtgatttc	atatgcgcga	2340
ttgctgatcc	ccatgtgtat	cactggcaaa	ctgtgatgga	cgacacgctc	agtgcgctccg	2400
tcgcgcaggc	tctcgatgag	ctgatgcttt	gggccgagga	ctgccccgaa	gtccggcacc	2460
tcgtgcacgc	ggatttcggc	tccaacaatg	tcttgacgga	caatggccgc	ataacagcgg	2520
tcattgactg	gagcgaggcg	atgttcgggg	attcccaata	cgaggtcgcc	aacatcttct	2580
tctggaggcc	gtggttggct	tgtatggagc	agcagacgcg	ctacttcgag	cggaggcatc	2640
cggagcttgc	aggatcgccg	cggctccggg	cgtatatgct	ccgcattggg	cttgaccaac	2700
tctatcagag	cttggttgac	ggcaatttcg	atgatgcagc	ttgggcgcag	ggtcgatgcg	2760
acgcaatcgt	ccgatccgga	gccgggactg	tcgggcgtac	acaaatcgcc	cgcagaagcg	2820
cggccgtctg	gaccgatggc	tgtgtagaag	tactcgccga	tagtggaaac	cgacgccccca	2880

gcactcgtcc gagggcaaag gaatagagta gatgccgacc gaacaagagc tgatttcgag	2940
aacgcctcag ccagcaactc gcgcgagcct agcaaggcaa atgcgagaga acggccttac	3000
gcttgggtggc acagttctcg tccacagttc gctaagctcg ctcggtggg tcgcgggagg	3060
gccggtcgca gtgattcagg ccttctgga ttgtgttggc cccagggca cgattgtcat	3120
gcccacgcac tcgggtgatc tgactgatcc cgcagattgg agatcgccgc ccgtgcctgc	3180
cgattgggtg cagatctaga gctcgctgat cagcctcgac tgtgcctcta gttgccagcc	3240
atctgttgtt tgccctccc ccgtgccttc cttgaccctg gaagggtgcca ctcccactgt	3300
cctttcctaa taaaatgagg aaattgcac gcattgtctg agtaggtgtc attctattct	3360
ggggggtggg gtggggcagg acagcaaggg ggaggattgg gaagacaata gcaggcatgc	3420
tggggatgcg gtgggctcta tggttctga ggcggaaaga accagctggg gctcgagtgc	3480
attctagttg tggtttgtcc aaactcatca atgtatctta tcatgtctgt ataccgtcga	3540
cctctagcta gagcttggcg taatcatggt catagctgtt tctgtgtga aattgttacc	3600
cgctcacaat tccacacaac atacgagccg gaagcataaa gtgtaaagcc tggggtgcct	3660
aatgagtgag ctaactcaca ttaattgcgt tgcgctcact gccgctttc cagtcgggaa	3720
acctgtcgtg ccagctgcat taatgaatcg gccaacgcgc ggggagaggc ggtttgcgta	3780
ttgggcgctc ttccgcttcc tcgctcactg actcgctgcg ctcggtcggt cggtgcggc	3840
gagcggatcc agctcactca aaggcggtaa tacggttacc cacagaatca ggggataacg	3900
caggaaagaa catgtgagca aaaggccagc aaaaggccag gaaccgtaaa aaggccgcgt	3960
tgctggcggt tttccatagg ctccgcccc ctgacgagca tcacaaaaat cgacgctcaa	4020
gtcagagggt gcgaaaccgc acaggactat aaagatacca ggcgtttccc cctggaagct	4080
ccctcgtagc ctctctgtt ccgaccctgc cgcttaccgg atacctgtcc gcctttctcc	4140
cttcgggaag cgtggcgctt tctcaatgct cacgctgtag gtatctcagt tcggtgtagg	4200
tcgttcgctc caagctgggc tgtgtgcacg aacccccgt tcagcccgac cgctgcgcct	4260
tatccggtaa ctatcgctt gagtccaacc cggtaaagaca cgacttatcg ccaactggcag	4320
cagccactgg taacaggatt agcagagcga ggtatgtagg cgggtgtaca gagttcttga	4380
agtgggtggc taactacggc tacactagaa ggacagtatt tggatatctgc gctctgctga	4440
agccagttac cttcggaaaa agagttggta gctcttgatc cggcaaacaa accaccgctg	4500
gtagcggtag tttttttgtt tgcaagcagc agattacgcg cagaaaaaaaa ggatctcaag	4560
aagatccttt gatcttttct acggggtctg acgctcagtg gaacgaaaac tcacgttaag	4620

ggatttttgg	catgagatta	tcaaaaagga	tcttcaccta	gatacctttta	aattaaaaat	4680
gaagtttttaa	atcaatctaa	agtatatatg	agtaaacttg	gtctgacagt	taaccaatgct	4740
taatcagtga	ggcacctatc	tcagcgatct	gtctattttcg	ttcatccata	gttgccctgac	4800
tccccgctcg	gtagataact	acgatacggg	agggcttacc	atctggcccc	agtgctgcaa	4860
tgataccgcg	agacccacgc	tcaccggctc	cagattttatc	agcaataaac	cagccagccg	4920
gaagggccga	gcgcagaagt	ggtcctgcaa	ctttatccgc	ctccatccag	tctattaatt	4980
gttgccggga	agctagagta	agtagttcgc	cagttaatatg	tttgcgcaac	gttggttgcca	5040
ttgctacagg	catcgtgggtg	tcacgctcgt	cgtttggtat	ggcttcattc	agctccgggtt	5100
cccaacgata	aaggcgagtt	acatgatccc	ccatggtgtg	caaaaaagcg	gttagctcct	5160
tcggctctcc	gatacgttgtc	agaagtaagt	tggccgcagt	gttatcactc	atggttatgg	5220
cagcactgca	taattctctt	actgtcatgc	catccgtaag	atgcttttct	gtgactgggtg	5280
agtactcaac	caagtcattc	tgagaatagt	gtatgcggcg	accgagttgc	tcttgcccg	5340
cgtcaatacg	ggataatacc	gcgccacata	gcagaacttt	aaaagtgtc	atcattggaa	5400
aacgttcttc	ggggcgaaaa	ctctcaagga	tcttaccgct	gttgagatcc	agttcgatgt	5460
aaccactcg	tgacccaac	tgatcttcag	catcttttac	tttcaccagc	gtttctgggt	5520
gagcaaaaac	aggaaggcaa	aatgccgcaa	aaaagggaat	aaggcgaca	cggaaatgtt	5580
gaatactcat	actcttctt	tttcaatatt	attgaagcat	ttatcagggt	tattgtctca	5640
tgagcggata	catatttgaa	tgtatttaga	aaaataaaca	aataggggtt	ccgcgcacat	5700
ttccccgaaa	agtgccacct	gacgtc				5726

<210> 46
 <211> 456
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (334)..(334)
 <223> n is a, c, g, or t

<220>
 <221> misc_feature
 <222> (442)..(442)
 <223> n is a, c, g, or t

<400> 46

ccttttgagg taaactcctg tttttaataa tattttctaa aagttctgca attgcagcat	60
tgagaggtag aaacttttct catcaaactc ctgagcacta atctgcttac agtatgagta	120
agttggcaaa ggagcaaata gtccatctcc aggattttca atatgtccct tttttaagta	180
gtcaagatgt ttttccactg cagtctgtaa gtaagagggg acttgaagaa tttcctgatg	240
atgatccatt aagaaagaaa ctaatcttcc agcaagaagc tcatcaagat ccacttcttc	300
agcacagcat aacacacatc gagaaaaggt atgnatcatc aagtgacctc gtaccattg	360
catcatggaa gtttgggcat atccaccatt tttgactcat tcggggaaat catacgcat	420
aaaagtttga agcttctacg antttggttg ggggaa	456

<210> 47
 <211> 459
 <212> DNA
 <213> Homo sapiens

<400> 47	
gaacttgtga aaatcaataa aatgatttat tttatatatg caaaatcaaa atctctttgt	60
acactttaat ttttgcaaat tcatacaaac ataacaatac tgctccatat aaacttttgt	120
ataaacatta aaggaaatat acacatattt tgttcttctt gtgcttccaa agcacagaat	180
gtataagtcc atctgaagac tttctatcat cacatgcaag aacaaatgtc agaggttggg	240
ggcagcctca agtgcacttt gtaatgtctc ttctcaaggt actgaattag gactcgtctt	300
ttaaacccttg cggcttctct gatggtaaatt tcaacaaact gtttcttcat ctccagaggt	360
ccttgcactt cttcaagcaa aatgaaaatt ctttcatatt ttcgaccaa ctttcgaact	420
tccttcatta attgatggtt tatatcagca ttggattcc	459